

Andres

#18

Page 1 of 7

1646

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/394,020A

DATE: 07/18/2000  
TIME: 13:52:13

Input Set : A:\SeqLstg.txt  
Output Set: N:\CRF3\07182000\I394020A.raw

ENTERED

RECEIVED

AUG 02 2000

TECH CENTER 1600/2900

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: Pepicelli, Carmen V  
7 Lewis, Paula M  
8 McMahon, Andrew P  
10 (ii) TITLE OF INVENTION: Regulation of Lung Tissue by  
11 Hedgehog-like Polypeptides, and Formulations and Uses  
12 Related Thereto  
14 (iii) NUMBER OF SEQUENCES: 24  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: Foley, Hoag & Eliot, LLP  
18 (B) STREET: One Post Office Square  
19 (C) CITY: Boston  
20 (D) STATE: MA  
21 (E) COUNTRY: USA  
22 (F) ZIP: 02109  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: ASCII(text)  
C--> 30 (vi) CURRENT APPLICATION DATA:  
C--> 31 (A) APPLICATION NUMBER: US/09/394,020A  
C--> 32 (B) FILING DATE: 10-Sep-1999  
33 (C) CLASSIFICATION:  
35 (vii) PRIOR APPLICATION DATA:  
C--> 36 (A) APPLICATION NUMBER: US 60/099,952  
C--> 37 (B) FILING DATE: 11-SEP-1998  
39 (viii) ATTORNEY/AGENT INFORMATION:  
40 (A) NAME: Vincent, Matthew P  
41 (B) REGISTRATION NUMBER: 36,709  
42 (C) REFERENCE/DOCKET NUMBER: HUV-032.01  
44 (ix) TELECOMMUNICATION INFORMATION:  
45 (A) TELEPHONE: (617) 832-1000  
46 (B) TELEFAX: (617) 832-7000  
48 (2) INFORMATION FOR SEQ ID NO: 1:  
49 (i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 1277 base pairs  
51 (B) TYPE: nucleic acid  
52 (C) STRANDEDNESS: both  
53 (D) TOPOLOGY: linear  
55 (ii) MOLECULE TYPE: cDNA  
57 (ix) FEATURE:  
58 (A) NAME/KEY: CDS  
59 (B) LOCATION: 1..1275  
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
63 ATG GTC GAA ATG CTG CTG TTG ACA AGA ATT CTC TTG GTG GGC TTC ATC

48

RAW SEQUENCE LISTING                      DATE: 07/18/2000  
 PATENT APPLICATION: US/09/394,020A        TIME: 13:52:13

Input Set : A:\SeqLstg.txt  
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64 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
65   1           5           10           15
67 TGC GCT CTT TTA GTC TCC TCT GGG CTG ACT TGT GGA CCA GGC AGG GGC      96
68 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
69   20           25           30
71 ATT GGA AAA AGG AGG CAC CCC AAA AAG CTG ACC CCG TTA GCC TAT AAG      144
72 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
73   35           40           45
75 CAG TTT ATT CCC AAT GTG GCA GAG AAG ACC CTA GGG GCC AGT GGA AGA      192
76 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
77   50           55           60
79 TAT GAA GGG AAG ATC ACA AGA AAC TCC GAG AGA TTT AAA GAA CTA ACC      240
80 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
81  65           70           75           80
83 CCA AAT TAC AAC CCT GAC ATT ATT TTT AAG GAT GAA GAG AAC ACG GGA      288
84 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
85   85           90           95
87 GCT GAC AGA CTG ATG ACT CAG CGC TGC AAG GAC AAG CTG AAT GCC CTG      336
88 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
89  100          105          110
91 GCG ATC TCG GTG ATG AAC CAG TGG CCC GGG GTG AAG CTG CGG GTG ACC      384
92 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
93  115          120          125
95 GAG GGC TGG GAC GAG GAT GGC CAT CAC TCC GAG GAA TCG CTG CAC TAC      432
96 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
97  130          135          140
99 GAG GGT CGC GCC GTG GAC ATC ACC ACG TCG GAT CGG GAC CGC AGC AAG      480
100 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
101 145          150          155          160
103 TAC GGA ATG CTG GCC CGC CTC GCC GTC GAG GCC GGC TTC GAC TGG GTC      528
104 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
105 165          170          175
107 TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC      576
108 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
109 180          185          190
111 TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG      624
112 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
113 195          200          205
115 CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG      672
116 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
117 210          215          220
119 GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC      720
120 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
121 225          230          235          240
123 TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC      768
124 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
125 245          250          255
127 GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC      816
128 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala

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RAW SEQUENCE LISTING                      DATE: 07/18/2000  
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Input Set : A:\SeqLstg.txt  
 Output Set: N:\CRF3\07182000\I394020A.raw

129		260		265		270	
131	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG						864
132	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly						
133		275		280		285	
135	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA						912
136	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln						
137		290		295		300	
139	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT						960
140	Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser						
141	305		310		315		320
143	GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA						1008
144	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro						
145		325		330		335	
147	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC						1056
148	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys						
149		340		345		350	
151	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA						1104
152	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro						
153		355		360		365	
155	TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGC GCC						1152
156	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala						
157		370		375		380	
159	ATC CCT ACT GCC GCC ACC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG						1200
160	Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg						
161	385		390		395		400
162	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT						1248
163	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His						
164		405		410		415	
166	CCG CTG GGC ATG GTG GCA CCG GCC AGC TG						1277
167	Pro Leu Gly Met Val Ala Pro Ala Ser						
168		420		425			
171	(2) INFORMATION FOR SEQ ID NO: 2:						
173	(i) SEQUENCE CHARACTERISTICS:						
174	(A) LENGTH: 1190 base pairs						
175	(B) TYPE: nucleic acid						
176	(C) STRANDEDNESS: both						
177	(D) TOPOLOGY: linear						
179	(ii) MOLECULE TYPE: cDNA						
181	(ix) FEATURE:						
182	(A) NAME/KEY: CDS						
183	(B) LOCATION: 1..1191						
185	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
187	ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG						48
188	Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu						
189	1		5		10		15
191	GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG						96
192	Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg						
193		20		25		30	
195	CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT						144

## RAW SEQUENCE LISTING

DATE: 07/18/2000

PATENT APPLICATION: US/09/394,020A

TIME: 13:52:14

Input Set : A:\Seq1stg.txt

Output Set: N:\CRF3\07182000\I394020A.raw

196	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	Lys	Gln	Phe	
197			35					40					45				
199	GTG	CCC	AGT	ATG	CCC	GAG	CGG	ACC	CTG	GGC	GCG	AGT	GGG	CCA	GCG	GAG	192
200	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	Gly	Pro	Ala	Glu	
201		50					55					60					
203	GGG	AGG	GTA	ACA	AGG	GGG	TCG	GAG	CGC	TTC	CGG	GAC	CTC	GTA	CCC	AAC	240
204	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	Asp	Leu	Val	Pro	Asn	
205	65					70				75						80	
207	TAC	AAC	CCC	GAC	ATA	ATC	TTC	AAG	GAT	GAG	GAG	AAC	AGC	GGC	GCA	GAC	288
208	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Ser	Gly	Ala	Asp	
209					85					90				95			
211	CGC	CTG	ATG	ACA	GAG	CGT	TGC	AAA	GAG	CGG	GTG	AAC	GCT	CTA	GCC	ATC	336
212	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	Arg	Val	Asn	Ala	Leu	Ala	Ile	
213				100					105					110			
215	GCG	GTG	ATG	AAC	ATG	TGG	CCC	GGA	GTA	CGC	CTA	CGT	GTG	ACT	GAA	GGC	384
216	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
217			115					120					125				
219	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCA	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
220	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
221		130					135					140					
223	CGT	GCC	TTG	GAC	ATC	ACC	ACG	TCT	GAC	CGT	GAC	CGT	AAT	AAG	TAT	GGT	480
224	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
225	145					150				155						160	
227	TTG	TTG	GCG	CGC	CTA	GCT	GTG	GAA	GCC	GGA	TTC	GAC	TGG	GTC	TAC	TAC	528
228	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
229					165					170					175		
231	GAG	TCC	CGC	AAC	CAC	ATC	CAC	GTA	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
232	Glu	Ser	Arg	Asn	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
233				180					185					190			
235	GCG	GTC	CGA	GCC	GGC	TGC	TTT	CCG	GGA	AAT	GCC	ACG	GTG	CGC	TTG		624
236	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
237			195				200					205					
239	CGG	AGC	GGC	GAA	CGG	AAG	GGG	CTG	AGG	GAA	CTA	CAT	CGT	GGT	GAC	TGG	672
240	Arg	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
241		210					215					220					
243	GTA	CTG	GCC	GCT	GAT	GCA	GCG	GGC	CGA	GTG	GTA	CCC	ACG	CCA	GTG	CTG	720
244	Val	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
245	225					230					235					240	
247	CTC	TTC	CTG	GAC	CGG	GAT	CTG	CAG	CGC	CGC	GCC	TCG	TTC	GTG	GCT	GTG	768
248	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
249					245					250					255		
251	GAG	ACC	GAG	CGG	CCT	CCG	CGC	AAA	CTG	TTG	CTC	ACA	CCC	TGG	CAT	CTG	816
252	Glu	Thr	Glu	Arg	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
253				260					265						270		
255	GTG	TTC	GCT	GCT	CGC	GGG	CCA	GCG	CCT	GCT	CCA	GGT	GAC	TTT	GCA	CCG	864
256	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
257			275					280					285				
259	GTG	TTC	GCG	CGC	CGC	TTA	CGT	GCT	GGC	GAC	TCG	GTG	CTG	GCT	CCC	GGC	912
260	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/394,020A  
 DATE: 07/18/2000  
 TIME: 13:52:14

Input Set : A:\SeqListg.txt  
 Output Set: N:\CRF3\07182000\I394020A.raw

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261      290      295      300
263 GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA      960
264 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
265 305      310      315      320
267 GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC      1008
268 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
269      325      330      335
271 AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG      1056
272 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
273      340      345      350
275 GCC CAC CGC GCC TTC GCC CCT TTG CCG CTG CTG CAC GCG CTC GGG GCT      1104
276 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
277      355      360      365
279 CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT      1152
280 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
281      370      375      380
283 CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG      1190
284 Arg Leu Leu Tyr Arg Leu Ala Glu Leu Met Gly
285 385      390      395
288 (2) INFORMATION FOR SEQ ID NO: 3:
290 (i) SEQUENCE CHARACTERISTICS:
291 (A) LENGTH: 1281 base pairs
292 (B) TYPE: nucleic acid
293 (C) STRANDEDNESS: both
294 (D) TOPOLOGY: linear
296 (ii) MOLECULE TYPE: cDNA
299 (ix) FEATURE:
300 (A) NAME/KEY: CDS
301 (B) LOCATION: 1..1233
303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
305 ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG      48
306 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
307 1      5      10      15
309 CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG      96
310 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
311      20      25      30
313 GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC      144
314 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
315      35      40      45
317 TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC      192
318 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
319      50      55      60
321 GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG      240
322 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
323      65      70      75      80
325 CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC      288
326 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
327      85      90      95
329 ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC      336

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## VERIFICATION SUMMARY

DATE: 07/18/2000

PATENT APPLICATION: US/09/394,020A

TIME: 13:52:15

Input Set : A:\SeqLstg.txt

Output Set: N:\CRF3\07182000\I394020A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:36 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:  
L:37 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:  
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:2287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2385 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23, Value=[not relevant]